AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

On page 5, please amend the second and third full paragraphs:

FIG. 9 is the nucleotide sequence of the wMUC-1(6) vector (SEQ ID NO: 41).

FIG. 10 is the amino acid ~~nucleotide~~ sequence of wMUC-1(6) (SEQ ID NO: 42).

On page 10, second full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule does not have a sequence as described in FIG. 10.

On page 10, third full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule has a sequence as described in FIG. 10.

On page 11, first full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule does not have about a 30 ~~nucleotide~~ amino acid portion of consecutive ~~nucleotides~~ amino acids of a sequence a sequence as described in FIG. 10.

On page 11, third full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule has a sequence as described in FIG. 10.

On page 24, first full paragraph, please amend the specification as follows:

Sequence similarity searches can be also performed manually or by using several available computer programs known to those skilled in the art. Preferably, Blast and Smith-Waterman algorithms, which are available and known to those skilled in the art, and the like can be used. Blast is NCBI's sequence similarity search tool designed to support analysis of nucleotide and protein sequence databases. The GCG Package

provides a local version of Blast that can be used either with public domain databases or with any locally available searchable database. GCG Package v9.0 is a commercially available software package that contains over 100 interrelated software programs that enables analysis of sequences by editing, mapping, comparing and aligning them. Other programs included in the GCG Package include, for example, programs which facilitate RNA secondary structure predictions, nucleic acid fragment assembly, and evolutionary analysis. In addition, the most prominent genetic databases (GenBank, EMBL, PIR, and SWISS-PROT) are distributed along with the GCG Package and are fully accessible with the database searching and manipulation programs. GCG can be accessed through the Internet at, for example, ~~http://~~www.gcg.com/. Fetch is a tool available in GCG that can get annotated GenBank records based on accession numbers and is similar to Entrez. Another sequence similarity search can be performed with GeneWorld and GeneThesaurus from Pangea. GeneWorld 2.5 is an automated, flexible, high-throughput application for analysis of polynucleotide and protein sequences. GeneWorld allows for automatic analysis and annotations of sequences. Like GCG, GeneWorld incorporates several tools for sequence identity searching, gene finding, multiple sequence alignment, secondary structure prediction, and motif identification. GeneThesaurus 1.0™ is a sequence and annotation data subscription service providing information from multiple sources, providing a relational data model for public and local data.

On page 74, Table 1:

Peptide	Amino acid Position in MUC-1	Sequence	Predicted binding to HLA-A2*	T2 binding#	SEQ ID NO:
P-92	92-101	ATWGQDVTSV	POS	740	1
P-94	94-103	WGQDVTSVPV	NEG	591	8
P-1108	1108-1117	REGTINVHDV	NEG	482	9
P-4	4-13	GTQSPFFLLL	NEG	467	10
P-1105	1105-1114	LAFREGTINV	NEG	461	11

P-1104	1004-1013	TLASHSTKTD	NEG	442	12
P-1069	1069-1078	LQRDISEMFL	NEG	433	13
P-1162	1162-1171	ALLVLVCVLV	POS	431	3
P-1135	1135-1144	TISDVSVSDV	POS	422	4
P-1172	1173-1181	ALAIVYLIAL	POS	372	5
P-1169	1169-1178	VLVALAIVYL	POS	369	6
P-1177	1177-1186	LIALAVCQC	POS	338	7
CAP1-6D	NA	YLSGADLNL	POS	975	38
NCA	NA	YRPGENLNL	NEG	365	39

*Predicted binding on the basis of reported motif (37); POS = positive; NEG = negative.

#Results are expressed in relative fluorescence. CAP1-6D is an HLA-A2 binding carcinoembryonic antigen peptide that was used as a positive control. NCA peptide was used as a negative control.

NA = not applicable.

On page 84, first full paragraph:

HLA-A2 binding peptides used included: (a) the CEA agonist peptide CAP1-6D (YLSGADLNL) (SEQ ID NO: 38), designated CEA peptide, (b) the MUC-1 agonist peptide P-93L (ALWGQDVTSV) (SEQ ID NO: 2), designated MUC-1 peptide, (c) the prostate-specific antigen (PSA) peptide PSA-3 (VISNDVCAQV) (SEQ ID NO: 40). All peptides were greater than 96% pure and manufactured by American Peptide Company, Inc. (Sunnyvale, Calif.).

In the paragraph bridging pages 87-88:

Cultures were then incubated for 3 days at 37° C. in a humidified atmosphere containing 5% CO_2. After removal of the peptide containing medium, the cultures were supplemented with recombinant human IL-2 at a concentration of 20 units/ml for 7 days. T-cell lines from patients 55, 49 and 41 were generated by stimulation of PBMCs with autologous DCs infected with rF-CEA/MUC/TRICOM, using the same stimulation protocol described above. Patient 55 initially underwent a Whipple procedure for localized pancreatic cancer followed by adjuvant radiation therapy to the pancreatic bed. The patient had local recurrence and received chemotherapy with 5FU/Leucovorin

followed by an experimental vaccine study using both vaccinia-CEA and ALVAC-CEA prior to enrolling on this clinical trial. Patient 41 was diagnosed with colorectal carcinoma with liver metastasis. Prior to enrolling on study, this patient progressed on three different chemotherapy regimens, including 5FU/Leucovorin/CPT-11, 5FU/Leucovorin/Oxalliplatin, and ~~Xeloda~~ XELODA™ (Capecitabine). Patient 49 had colorectal cancer with both liver and lung metastasis. The patient progressed following four cycles of chemotherapy with CPT-11/5FU/Leucovorin prior to enrolling on study.